Application No: 10595585   Version No: 1.0

Input Set:

Output Set:

Started: 2008-07-22 21:11:18.188
Finished: 2008-07-22 21:11:19.445
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 257 ms
Total Warnings: 21
Total Errors: 0
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started:	2008-07-22 21:11:18.188
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Total Errors:	0
No. of SeqIDs Defined:	21
Actual SeqID Count:	21

Error code   Error Description

This error has occured more than 20 times, will not be displayed

<110>   YANG, Beom-Seok
           PARK, Sung-Dae

<120>   DDR2 PROTEIN WITH ACTIVATED KINASE ACTIVITY
           AND PREPARATION METHOD THEREOF

<130>   300602005700

<140>   10595585
<141>   2008-07-22

<150>   PCT/KR2004/002784
<151>   2004-11-01

<150>   KR10-2003-0076967
<151>   2003-10-31

<160>   21

<170>   KopatentIn 1.71

<210>   1
<211>   855
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Human DDR2 protein synthetic construct

<400>   1
Met Ile Leu Ile Pro Arg Met Leu Leu Val Leu Phe Leu Leu Leu Pro
  1   5   10   15

Ile Leu Ser Ser Ala Lys Ala Gln Val Asn Pro Ala Ile Cys Arg Tyr
              20   25   30

Pro Leu Gly Met Ser Gly Gly Gln Ile Pro Asp Glu Asp Ile Thr Ala
          35   40   45

Ser Ser Gln Trp Ser Glu Ser Thr Ala Ala Lys Tyr Gly Arg Leu Asp
      50   55   60

Ser Glu Glu Gly Asp Gly Ala Trp Cys Pro Glu Ile Pro Val Glu Pro
  65   70   75   80

Asp Asp Leu Lys Glu Phe Leu Gln Ile Asp Leu His Thr Leu His Phe
                  85   90   95

Ile Thr Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly His Gly Ile
              100   105   110

Glu Phe Ala Pro Met Tyr Lys Ile Asn Tyr Ser Arg Asp Gly Thr Arg
              115   120   125

Trp Ile Ser Trp Arg Asn Arg His Gly Lys Gln Val Leu Asp Gly Asn

```
                130                    135                    140


Ser Asn Pro Tyr Asp Ile Phe Leu Lys Asp Leu Glu Pro Pro Ile Val
145                    150                    155                    160


Ala Arg Phe Val Arg Phe Ile Pro Val Thr Asp His Ser Met Asn Val
                    165                    170                    175


Cys Met Arg Val Glu Leu Tyr Gly Cys Val Trp Leu Asp Gly Leu Val
                    180                    185                    190


Ser Tyr Asn Ala Pro Ala Gly Gln Gln Phe Val Leu Pro Gly Gly Ser
                195                    200                    205


Ile Ile Tyr Leu Asn Asp Ser Val Tyr Asp Gly Ala Val Gly Tyr Ser
210                    215                    220


Met Thr Glu Gly Leu Gly Gln Leu Thr Asp Gly Val Ser Gly Leu Asp
225                    230                    235                    240


Asp Phe Thr Gln Thr His Glu Tyr His Val Trp Pro Gly Tyr Asp Tyr
                    245                    250                    255


Val Gly Trp Arg Asn Glu Ser Ala Thr Asn Gly Tyr Ile Glu Ile Met
                260                    265                    270


Phe Glu Phe Asp Arg Ile Arg Asn Phe Thr Thr Met Lys Val His Cys
                275                    280                    285


Asn Asn Met Phe Ala Lys Gly Val Lys Ile Phe Lys Glu Val Gln Cys
290                    295                    300


Tyr Phe Arg Ser Glu Ala Ser Glu Trp Glu Pro Asn Ala Ile Ser Phe
305                    310                    315                    320


Pro Leu Val Leu Asp Asp Val Asn Pro Ser Ala Arg Phe Val Thr Val
                    325                    330                    335


Pro Leu His His Arg Met Ala Ser Ala Ile Lys Cys Gln Tyr His Phe
                    340                    345                    350


Ala Asp Thr Trp Met Met Phe Ser Glu Ile Thr Phe Gln Ser Asp Ala
        355                    360                    365


Ala Met Tyr Asn Asn Ser Glu Ala Leu Pro Thr Ser Pro Met Ala Pro
        370                    375                    380


Thr Thr Tyr Asp Pro Met Leu Lys Val Asp Asp Ser Asn Thr Arg Ile
385                    390                    395                    400


Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile Leu Leu Ala Ile Ile
                    405                    410                    415


Val Ile Ile Leu Trp Arg Gln Phe Trp Gln Lys Met Leu Glu Lys Ala
                420                    425                    430


Ser Arg Arg Met Leu Asp Asp Glu Met Thr Val Ser Leu Ser Leu Pro
```

Ser Asp Ser Ser Met Phe Asn Asn Asn Arg Ser Ser Ser Pro Ser Glu
    450   455   460

Gln Gly Ser Asn Ser Thr Tyr Asp Arg Ile Phe Pro Leu Arg Pro Asp
465   470   475   480

Tyr Gln Glu Pro Ser Arg Leu Ile Arg Lys Leu Pro Glu Phe Ala Pro
                485   490   495

Gly Glu Glu Glu Ser Gly Cys Ser Gly Val Val Lys Pro Val Gln Pro
            500   505   510

Ser Gly Pro Glu Gly Val Pro His Tyr Ala Glu Ala Asp Ile Val Asn
        515   520   525

Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ser Val Pro Ala Val Thr
    530   535   540

Met Asp Leu Leu Ser Gly Lys Asp Val Ala Val Glu Glu Phe Pro Arg
545   550   555   560

Lys Leu Leu Thr Phe Lys Glu Lys Leu Gly Glu Gly Gln Phe Gly Glu
                565   570   575

Val His Leu Cys Glu Val Glu Gly Met Glu Lys Phe Lys Asp Lys Asp
            580   585   590

Phe Ala Leu Asp Val Ser Ala Asn Gln Pro Val Leu Val Ala Val Lys
        595   600   605

Met Leu Arg Ala Asp Ala Asn Lys Asn Ala Arg Asn Asp Phe Leu Lys
    610   615   620

Glu Ile Lys Ile Met Ser Arg Leu Lys Asp Pro Asn Ile Ile His Leu
625   630   635   640

Leu Ser Val Cys Ile Thr Asp Asp Pro Leu Cys Met Ile Thr Glu Tyr
                645   650   655

Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser Arg His Glu Pro Pro
            660   665   670

Asn Ser Ser Ser Ser Asp Val Arg Thr Val Ser Tyr Thr Asn Leu Lys
        675   680   685

Phe Met Ala Thr Gln Ile Ala Ser Gly Met Lys Tyr Leu Ser Ser Leu
    690   695   700

Asn Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Lys
705   710   715   720

Asn Tyr Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr
                725   730   735

Ser Gly Asp Tyr Tyr Arg Ile Gln Gly Arg Ala Val Leu Pro Ile Arg

```
                740                          745                          750
Trp Met Ser Trp Glu Ser Ile Leu Leu Gly Lys Phe Thr Thr Ala Ser
        755                  760                  765

Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Thr Phe Thr Phe Cys
    770                  775                  780

Gln Glu Gln Pro Tyr Ser Gln Leu Ser Asp Glu Gln Val Ile Glu Asn
785                  790                  795                  800

Thr Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Thr Tyr Leu Pro Gln
                805                  810                  815

Pro Ala Ile Cys Pro Asp Ser Val Tyr Lys Leu Met Leu Ser Cys Trp
        820                  825                  830

Arg Arg Asp Thr Lys Asn Arg Pro Ser Phe Gln Glu Ile His Leu Leu
        835                  840                  845

Leu Leu Gln Gln Gly Asp Glu
    850                  855
```

<210>   2
<211>   22
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Human DDR2 protein transmembrane domain synthetic construct
         (400~420)

<400>   2
```
Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile Leu Leu Ala Ile
  1               5                   10                  15

Ile Val Ile Ile Leu Trp
                20
```

<210>   3
<211>   415
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Human DDR2 protein C-terminal tyrosine kinase active
         domain synthetic construct (441~855)

<400>   3
```
Met Thr Val Ser Leu Ser Leu Pro Ser Asp Ser Ser Met Phe Asn Asn
  1               5                   10                  15

Asn Arg Ser Ser Ser Pro Ser Glu Gln Gly Ser Asn Ser Thr Tyr Asp
```

Arg Ile Phe Pro Leu Arg Pro Asp Tyr Gln Glu Pro Ser Arg Leu Ile
        35   40   45

Arg Lys Leu Pro Glu Phe Ala Pro Gly Glu Glu Glu Ser Gly Cys Ser
        50   55   60

Gly Val Val Lys Pro Val Gln Pro Ser Gly Pro Glu Gly Val Pro His
65   70   75   80

Tyr Ala Glu Ala Asp Ile Val Asn Leu Gln Gly Val Thr Gly Gly Asn
                85   90   95

Thr Tyr Ser Val Pro Ala Val Thr Met Asp Leu Leu Ser Gly Lys Asp
                100   105   110

Val Ala Val Glu Glu Phe Pro Arg Lys Leu Leu Thr Phe Lys Glu Lys
        115   120   125

Leu Gly Glu Gly Gln Phe Gly Glu Val His Leu Cys Glu Val Glu Gly
        130   135   140

Met Glu Lys Phe Lys Asp Lys Asp Phe Ala Leu Asp Val Ser Ala Asn
145   150   155   160

Gln Pro Val Leu Val Ala Val Lys Met Leu Arg Ala Asp Ala Asn Lys
                165   170   175

Asn Ala Arg Asn Asp Phe Leu Lys Glu Ile Lys Ile Met Ser Arg Leu
                180   185   190

Lys Asp Pro Asn Ile Ile His Leu Leu Ser Val Cys Ile Thr Asp Asp
        195   200   205

Pro Leu Cys Met Ile Thr Glu Tyr Met Glu Asn Gly Asp Leu Asn Gln
        210   215   220

Phe Leu Ser Arg His Glu Pro Pro Asn Ser Ser Ser Ser Asp Val Arg
225   230   235   240

Thr Val Ser Tyr Thr Asn Leu Lys Phe Met Ala Thr Gln Ile Ala Ser
                245   250   255

Gly Met Lys Tyr Leu Ser Ser Leu Asn Phe Val His Arg Asp Leu Ala
                260   265   270

Thr Arg Asn Cys Leu Val Gly Lys Asn Tyr Thr Ile Lys Ile Ala Asp
        275   280   285

Phe Gly Met Ser Arg Asn Leu Tyr Ser Gly Asp Tyr Tyr Arg Ile Gln
        290   295   300

Gly Arg Ala Val Leu Pro Ile Arg Trp Met Ser Trp Glu Ser Ile Leu
305   310   315   320

Leu Gly Lys Phe Thr Thr Ala Ser Asp Val Trp Ala Phe Gly Val Thr

```
                325                  330                  335

Leu Trp Glu Thr Phe Thr Phe Cys Gln Glu Gln Pro Tyr Ser Gln Leu
         340                  345                  350


Ser Asp Glu Gln Val Ile Glu Asn Thr Gly Glu Phe Phe Arg Asp Gln
      355                  360                  365


Gly Arg Gln Thr Tyr Leu Pro Gln Pro Ala Ile Cys Pro Asp Ser Val
   370                  375                  380


Tyr Lys Leu Met Leu Ser Cys Trp Arg Arg Asp Thr Lys Asn Arg Pro
385                  390                  395                  400


Ser Phe Gln Glu Ile His Leu Leu Leu Leu Gln Gln Gly Asp Glu
                405                  410                  415



<210>    4
<211>    1608
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Full-length src c-DNA synthetic construct


<400>    4
atgggcagca acaagagcaa gcccaaggac gccagccagc ggcgccgcag cctggagccc        60

tcggaaaacg tgcacggggc agggggcgcc ttcccggcct cacagacacc gagcaagccc       120

gcctccgccg acggccaccg cgggcccagc gccgccttcg tgccgcccgc ggccgagccc       180

aagctcttcg gaggcttcaa ctcctcggac accgtcacct ccccgcagag ggcggggggct      240

ctggcaggtg gggtgaccac ctttgtggcc ctctatgact atgagtcacg gacagagact       300

gacctgtcct tcaagaaagg ggagcggctg cagattgtta caaacacgga gggagactgg       360

tggctggcac actcgctgag cacgggacag accggttaca tccccagcaa ctatgtggcg       420

ccctccgact ccatccaggc tgaggagtgg tactttggta agatcactag acgagaatca       480

gagcggctgc tgctcaacgc cgagaacccg agagggacct tcctcgtgag ggagagtgag       540

accacaaaag gtgcctactg cctctctgta tccgacttcg acaatgccaa gggtctaaat       600

gtgaaacact acaagatccg caagctggac agcggcggtt tctacatcac ctcccgcacc       660

cagttcaaca gcctgcagca gctcgtggct tactactcca acatgctgat ggcctgtgt        720

caccgcctca ctaccgtatg tcccacatcc aagcctcaga cccagggatt ggccaaggat       780

gcgtgggaga tccccccggga gtccctgcgg ctggaggtca agctgggcca gggttgcttc       840

ggagaggtgt ggatggggac ctggaacggc accacgaggg ttgccatcaa aactctgaag       900
```

```
ccaggcacca tgtccccaga ggccttcctg caggaggccc aagtcatgaa gaaactgagg          960

cacgagaaac tggtgcagct gtatgctgtg gtgtcggaag aacccattta cattgtgaca         1020

gagtacatga acaaggggag tctgctggac tttctcaagg gggaaacggg caaatatttg         1080

cggctacccc agctggtgga catgtctgct cagatcgctt caggcatggc ctatgtggag         1140

cggatgaact atgtgcaccg ggaccttcga gccgccaata tcctagtagg ggagaacctg         1200

gtgtgcaaag tggccgactt tgggttggcc cggctcatag aagacaacga atacacagcc         1260

cggcaaggtg ccaaattccc catcaagtgg accgcccctg aagctgctct gtacggcagg         1320

ttcaccatca gtcggatgt gtggtccttt gggattctgc tgaccgagct caccactaag         1380

ggaagagtgc cctatcctgg gatggtgaac cgtgaggttc tggaccaggt ggagcggggc         1440

taccggatgc cttgtccccc cgagtgcccc gagtccctgc atgaccttat gtgccagtgc         1500

tggcggaagg agcccgagga gcggcccacc ttcgagtacc tgcaggcctt cctggaagac         1560

tactttacgt ccactgagcc acagtaccag cccgggggaga acctatag                     1608


<210>      5
<211>      1449
<212>      DNA
<213>      Artificial Sequence

<220>
<223>      Full-length fyn gene synthetic construct


<400>      5
atgggctgtg tgcaatgtaa ggataaagaa gcaacaaaac tgacggagga gagggacggc           60

agcctgaacc agagctctgg gtaccgctat ggcacagacc ccacccctca gcactacccc          120

agcttcggtg tgacctccat ccccaactac aacaacttcc acgcagccgg gggccaagga          180

ctcaccgtct ttggaggtgt gaactcttcg tctcatacgg ggaccttgcg tacgagagga          240

ggaacaggag tgacactctt tgtggccctt tatgactatg aagcacggac agaagatgac          300

ctgagttttc acaaaggaga aaaatttcaa atattgaaca gctcggaagg agattggtgg          360

gaagcccgct ccttgacaac tggagagaca ggttacattc ccagcaatta tgtggctcca          420

gttgactcta tccaggcaga agagtggtac tttggaaaac ttggccgaaa agatgctgag          480

cgacagctat tgtcctttgg aaacccaaga ggtacctttc ttatccgcga gagtgaaacc          540

accaaaggtg cctattcact ttctatccgt gattgggatg atatgaaagg agaccatgtc          600

aaacattata aaattcgcaa acttgacaat ggtggatact acattaccac ccgggcccag          660
```

tttgaaacac ttcagcagct tgtacaacat tactcaggta cctggaatgg aaacacaaaa   720

gtagccataa agactcttaa accaggcaca atgtccccg aatcattcct tgaggaagcg   780

cagatcatga agaagctgaa gcacgacaag ctggtccagc tctatgcagt ggtgtctgag   840

gagcccatct acatcgtcac cgagtatatg aacaaaggaa gtttactgga tttcttaaaa   900

gatggagaag aagagctct gaaattacca aatcttgtgg acatggcagc acaggtggct   960

gcaggaatgg cttacatcga gcgcatgaat tatatccata gagatctgcg atcagcaaac   1020

attctagtgg ggaatggact catatgcaag attgctgact tcggattggc ccgattgata   1080

gaagacaatg agtacacagc aagacaaggt gcaaagttcc ccatcaagtg gacggccccc   1140

gaggcagccc tgtacgggag gttcacaatc aagtctgacg tgtggtcttt tggaatctta   1200

ctcacagagc tggtcaccaa aggaagagtg ccatacccag gcatgaacaa ccgggaggtg   1260

ctggagcagg tggagcgagg ctacaggatg ccctgcccgc aggactgccc catctctctg   1320

catgagctca tgatccactg ctggaaaaag gaccctgaag aacgccccac ttttgagtac   1380

ttgcagagct tcctggaaga ctactttacc gcgacagagc cccagtacca acctggtgaa   1440

aacctgtaa   1449

<210>   6
<211>   29
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   5' primer for PCR of DDR2 protein

<400>   6
cccggatcca tgacagtcag cctttccct   29

<210>   7
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   3' primer for PCR of DDR2 protein

<400>   7
gggtctagat cactcgtcgc cttgttgaag   30

<210>   8

<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   5' primer for PCR of human full-length src c-DNA

<400>   8
gggggattcg acggatcggg agatctcccg   30

<210>   9
<211>   33
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   3' primer for PCR of human full-length src c-DNA

<400>   9
cccgaattcg acgtcaggtg gcacttttcg ggg   33

<210>   10
<211>   18
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Forward primer containing Nco I site for mutation of K608A

<400>   10
gccgtcacca tggacctg   18

<210>   11
<211>   18
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Reverse primer containing Bam HI site for mutation of K608A

<400>   11
gcccggccct ggatccgg   18

<210>   12
<211>   21
<212>   DNA
<213>   Artificial Sequence

<220>

<223>   Forward primer containing K608A mutation

<400>   12
gtggctgtgg caatgctccg a   21

<210>   13
<211>   21
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Reverse primer containing K608A mutation

<400>   13
tcggagcatt gccacagcca c   21

<210>   14
<211>   20
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   5' primer containing Nco I site for tyrosine mutation

<400>   14
actcagtgcc tgccgtcacc   20

<210>   15
<211>   41
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   3' primer for mutation of Y740F

<400>   15
cccggccctg gatccggtaa tagtcaccac tgaacaggtt c